PCT10

RAW SEQUENCE LISTING   DATE: 11/18/2002
PATENT APPLICATION: **US/10/089,787**   TIME: 15:15:14

Input Set : **A:\20522p.txt**
Output Set: **N:\CRF4\11182002\J089787.raw**

```
  4 <110> APPLICANT: El-Sherbeini, Mohamed
  5         Azzolina, Barbara A.
  7 <120> TITLE OF INVENTION: MraY GENE AND ENZYME OF PSEUDOMONAS
  8         AERUGINOSA
 10 <130> FILE REFERENCE: 20522P
 12 <140> CURRENT APPLICATION NUMBER: 10/089,787
 13 <141> CURRENT FILING DATE: 2002-04-03
 15 <150> PRIOR APPLICATION NUMBER: PCT/US00/27056
 16 <151> PRIOR FILING DATE: 2000-09-29
 18 <150> PRIOR APPLICATION NUMBER: 60/157,580
 19 <151> PRIOR FILING DATE: 1999-10-04
 21 <160> NUMBER OF SEQ ID NOS: 4
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0           ENTERED
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1083
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Pseudomonas Aeruginosa
 30 <400> SEQUENCE: 1
 31 atgctcctgc tgctggccga atacctgcaa cagttctaca agggcttcgg cgtcttccag    60
 32 tacctgaccc tgcgcggcat tctcagcgtg ctcaccgcgc tgtcgctgtc gctgtggctg   120
 33 gggccctgga tgatccgtac cttgcagatc ccccagatcg gccaggccgt gcgcaacgac   180
 34 ggtccgcagt cgcacctgtc gaagaagggc accccgacca tgggcggcgc cctgatcctt   240
 35 accgccatag ccatcagcac gctgctgtgg gcggatcttt ccaaccgcta cgtgtgggta   300
 36 gtgctggtcg ttaccctgct gttcggtgcc atcggctggg tagacgacta ccgcaaggtg   360
 37 atcgagaaga actcccgtgg cctgccgagc cgctggaagt acttctggca gtcggtgttc   420
 38 ggcatcggcg ccgccgtgtt cctctacatg actgccgaaa ccccgatcga gaccaccctg   480
 39 atcgtgccga tgctgaagag cgtcgagatc cagttgggca tcttcttcgt ggtcctgacc   540
 40 tacttcgtca tcgtcggctc gagcaatgcg gtgaacctca ccgacggtct cgacggcctg   600
 41 gcgatcatgc cgacggtaat ggttgccggc gcgctgggca tcttctgcta cctgtcgggc   660
 42 aacgtgaagt tcgccgagta cctgctgatt cccaacgtac cgggcgccgg cgagctgatc   720
 43 gtgttctgcg ccgcgctggt cggcgccggc ctcggcttcc tctggttcaa cacctatccg   780
 44 gcgcaggtct tcatgggcga cgtcggcgcg ctggcgctgg cgccgcgct gggcaccatc   840
 45 gcggtgatcg tgcgccagga gatcgtgctg ttcatcatgg gtggggtgtt cgtcatggaa   900
 46 accctctcgg tgatgatcca ggtcgcttcc ttcaagctga ccggacgccg cgtcttccgt   960
 47 atggcgccga tccatcacca tttcgaactg aaaggctggc cggacccgcg cgtgatcgtg  1020
 48 cgcttctgga tcatcaccgt gatcctggtg ctgatcggcc tcgccacctt gaagctgcgt  1080
 49 tga                                                                1083
 51 <210> SEQ ID NO: 2
 52 <211> LENGTH: 360
 53 <212> TYPE: PRT
 54 <213> ORGANISM: Pseudomonas Aeruginosa
 56 <400> SEQUENCE: 2
 57 Met Leu Leu Leu Leu Ala Glu Tyr Leu Gln Gln Phe Tyr Lys Gly Phe
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```
 58   1                   5                   10                  15
 59  Gly Val Phe Gln Tyr Leu Thr Leu Arg Gly Ile Leu Ser Val Leu Thr
 60          20                  25                  30
 61  Ala Leu Ser Leu Ser Leu Trp Leu Gly Pro Trp Met Ile Arg Thr Leu
 62          35                  40                  45
 63  Gln Ile Pro Gln Ile Gly Gln Ala Val Arg Asn Asp Gly Pro Gln Ser
 64      50                  55                  60
 65  His Leu Ser Lys Lys Gly Thr Pro Thr Met Gly Gly Ala Leu Ile Leu
 66  65                  70                  75                  80
 67  Thr Ala Ile Ala Ile Ser Thr Leu Leu Trp Ala Asp Leu Ser Asn Arg
 68                  85                  90                  95
 69  Tyr Val Trp Val Val Leu Val Val Thr Leu Leu Phe Gly Ala Ile Gly
 70              100                 105                 110
 71  Trp Val Asp Asp Tyr Arg Lys Val Ile Glu Lys Asn Ser Arg Gly Leu
 72          115                 120                 125
 73  Pro Ser Arg Trp Lys Tyr Phe Trp Gln Ser Val Phe Gly Ile Gly Ala
 74      130                 135                 140
 75  Ala Val Phe Leu Tyr Met Thr Ala Glu Thr Pro Ile Glu Thr Thr Leu
 76  145                 150                 155                 160
 77  Ile Val Pro Met Leu Lys Ser Val Glu Ile Gln Leu Gly Ile Phe Phe
 78              165                 170                 175
 79  Val Val Leu Thr Tyr Phe Val Ile Val Gly Ser Ser Asn Ala Val Asn
 80              180                 185                 190
 81  Leu Thr Asp Gly Leu Asp Gly Leu Ala Ile Met Pro Thr Val Met Val
 82          195                 200                 205
 83  Ala Gly Ala Leu Gly Ile Phe Cys Tyr Leu Ser Gly Asn Val Lys Phe
 84      210                 215                 220
 85  Ala Glu Tyr Leu Leu Ile Pro Asn Val Pro Gly Ala Gly Glu Leu Ile
 86  225                 230                 235                 240
 87  Val Phe Cys Ala Ala Leu Val Gly Ala Gly Leu Gly Phe Leu Trp Phe
 88              245                 250                 255
 89  Asn Thr Tyr Pro Ala Gln Val Phe Met Gly Asp Val Gly Ala Leu Ala
 90              260                 265                 270
 91  Leu Gly Ala Ala Leu Gly Thr Ile Ala Val Ile Val Arg Gln Glu Ile
 92          275                 280                 285
 93  Val Leu Phe Ile Met Gly Gly Val Phe Val Met Glu Thr Leu Ser Val
 94      290                 295                 300
 95  Met Ile Gln Val Ala Ser Phe Lys Leu Thr Gly Arg Arg Val Phe Arg
 96  305                 310                 315                 320
 97  Met Ala Pro Ile His His His Phe Glu Leu Lys Gly Trp Pro Asp Pro
 98              325                 330                 335
 99  Arg Val Ile Val Arg Phe Trp Ile Ile Thr Val Ile Leu Val Leu Ile
100              340                 345                 350
101  Gly Leu Ala Thr Leu Lys Leu Arg
102          355                 360
104  <210> SEQ ID NO: 3
105  <211> LENGTH: 29
106  <212> TYPE: DNA
107  <213> ORGANISM: Artificial Sequence
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```
109 <220> FEATURE:
110 <223> OTHER INFORMATION: PCR Primer
112 <400> SEQUENCE: 3
113 ttcatatgct cctgctgctg gccgaatac                                29
115 <210> SEQ ID NO: 4
116 <211> LENGTH: 27
117 <212> TYPE: DNA
118 <213> ORGANISM: Artificial Sequence
120 <220> FEATURE:
121 <223> OTHER INFORMATION: PCR Primer
123 <400> SEQUENCE: 4
124 ttggatcctc aacgcagctt caaggtg                                  27
```

VERIFICATION SUMMARY
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